APPENDIX A

Sample Benchsheets

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Facility	Name:	

BOD₅ Benchsheet

Sample Locati Raw Final	on (specific)		Sample	Type (grab, xx	x hr Comp., etc.)	
Sample Date: Collected by:		<u></u>	Test Da Analyst			
Samples IN Room Temp (°C	Date: Time:		Samples Room T	OUT	Date:	
	ssure			tric pressure		
	Bottle #	Sample mLs	Initial DO (mg/L)	Final DO (mg/L)	Depletion (mg/L)	Comments
Blank						Depletion must be less than 0.2 mg/L
Seeded Blank						
Seed source:			Seed Co	rrection factor	(SCF):	

Sample	Bottle #	Sample mLs	Seed mLs added	Initial DO	Final DO	DO depletion	SCF	Dilution factor	BOD ₅ mg/L	¹ Average BOD ₅
		А		В	С	D=B-C	Е	F=300/A	F x (D-E)	
Raw										
Final										
GGA										
GGA										
Replicate										
of										

¹ Average only those values which are associated with a depletion of at least 2 mg/L and a final DO \geq 1 mg/L.

Calculation = $BOD_5 mg/L = [(B-C)-E] x F$

	TSS Benchsheet
Sample Location (specific) Raw Final	Sample Type (grab, xx hr Comp., etc.)
Sample Date:	Test Date: Analyst:
Samples IN Date:	Samples OUT Date:

		Influent	Effluent	Replicate	Other:	Other:
		(Raw)	(Final)	(of)		-
Crucible/filter ID						
¹ Volume Filtered (1	mLs)					
Crucible/Filter	1st weight					
AFTER drying	² 2 nd weight					
(g) or (mg)	² 3 rd weight					
Crucible/Filter	1st weight					
tare weight	² 2 nd weight					
(g) or (mg)	² 3 rd weight					
³ Weight of dry soli	ds (mg)					
⁴ TSS (mg/L)						

Oven Temp (°C)

Time:_____

Facility Name: _____

Oven Temp (°C)

Time: _____

¹ Filter sufficient volume of sample to capture at least 1 mg (0.001 g) of solids.

² If samples are dried overnight, then re-drying/re-weighing is not necessary. Otherwise, at least once each quarter, one sample must be dried/weighed, and the re-dried and re-weighed to demonstrate that a constant dry weight is achieved based on the drying time employed.

³ Milligrams (mg) = grams x 100. The weight of dry solids must be less than 200 milligrams (0.2 g) or the analysis must be repeated using an appropriately smaller volume.

⁴ TSS = weight of dry solids (mg) x 1,000 volume Filtered (mL)

Facility Name:						
		A	Ammonia	(by electrode) Be	enchsheet	
Sample Locat Raw Final	ion (specifi	c)			e (grab, xx hr Comp., etc.)	
Sample Date: _ Collected by: _				Test Date: Analyst:		_ _ _
Calibration by:	Se R	Direct Read) emi-logarithr elative milliv inear regress	nic paper: olts:			
For <u>all</u> calibrat For linear regre	essions- In Co	tercept = orrelation co	efficient (r)=	(must be (must be (must be) (sample mV x slope +	be ≥ 0.995)	
	For ALL	calibrations	, and the second	For linear regi	neccurate	
	Sta: Conce	ndard entration g/L)	Millivolts (mV)	Log ₁₀ of concentration ¹ (mg/L)	Regression concentration ² (mg/L)	
	ALL calib	rations must	be based on a	t least 3 standards		
	¹ Take the	log of the o	oncentration	on using the millivolts of	f the standards	
		Influent (I	Raw)	Effluent (Final)	Replicate (of)	Matrix Spike (of)
Distilled? (Y/N						
Dilution Factor]				
Millivolts (mV)						
* mg/L from cal						
** Final mg/L						
		determined	l directly from	the calibration. If there	was no dilution involved	(i.e., you used the same
volume of sa	mple as wa	is used for th	ne standards, th	nen this is also equal to the	he final ammonia concent	ration.

Dilution Factor = mLs used for standards mLs used for sample

^{**} Final concentration = mg/L from calibration X DF

Facility Name:					
	To	tal Phosph	orus Bench	sheet	
Sample Location (specars) Raw Final	ecific)		Sample Type (grab, xx hr Comp., etc.)	_ _ _ _
Sample Date:			Test Date: Analyst:		_ _ _
Color Development i Calibration by: Interna	n Method Blank? (Y/al (Direct Read): Graph paper: Linear regression:	N):	- - -		
For <u>all</u> calibrations-	Slope (per decade of concent Intercept = correlation coefficient		(must be less than	r consistency or significant ch the LOD) >0.995	anges)
_	ntration mg/L = [samp				
	For ALL calibrations Standard Concentration (mg? or mg/L?) Blank	For linear n Absorbance @ 880 nm	gressions Regression	\mathbf{n}^1	
	alibrations must be base			f the standards	
	Known Standard If no full calibration this de	Influen (Raw)	t Effluent (Final)	Replicate (of	Matrix Spike (of)
Sample Volume mLs Absorbance (after coloring)					
Absorbance (before coloring) Net Absorbance Dilution Factor (DF) * mg/L from calibration ** Final mg/L as P					
* This is the concentra	,			as no dilution involved (final phosphorus conce	
** Final concentration	$= \underline{mg}$ from calibration X	DF			

^{**} Final concentration = $\underset{L}{\underline{mg}}$ from calibration X DF L

Dilution Factor = $\underset{mLs \text{ digested for standards}}{\underline{mLs \text{ digested for sample}}}$ X $\underset{mLs \text{ colored for standards}}{\underline{mLs \text{ colored for sample}}}$

Facility Name:	·				
		Residua	l Chlorine E	Benchsheet	
Sample Location (specific) Sample Type: Sample Date/Time: Collected by:	<u>GRAB</u>	<u></u>	Test Da Analyst		
Re	Direct Read): emi-logarithn elative milliv near regressi	nic paper: olts:			
		of concentration) =	(m	ust be within –54 to –60	mV)
For linear regressions- In	-	efficient (r)=		(must be ≥ 0.995)	
Concentra	ntion = Inve	se/antilog of [sample mV x slo	pe + intercept	
For ALL	calibrations		. •	For linear regre	economic
Stand	lard Cl ₂ ent (mg/L)	Absorbance @ 515 nm	Millivolts (mV) electrode method	Log ₁₀ of concentration ¹ (mg/L)	Regression concentration ² (mg/L)
Blank				(mg/ L)	(mg/L)
¹ Take the	log of the c	oncentration	at least 3 standard	s olts/absorbance of the	standards
			Effluent (Final)	Other:	
	Absorbanc	e		3 4141.	
	Millivolts (
	Dilution Fa				
	* mg/L from				
* This is the concentration	** Final mg		 he calibration If	there was no dilution it	

Dilution Factor = <u>mLs used for standards</u> mLs used for sample

^{*} This is the concentration determined directly from the calibration. If there was no dilution involved (i.e., you used the same volume of sample as was used for the standards, then this is also equal to the final ammonia concentration.

^{**} Final concentration = mg/L from calibration X DF

Facility Name:				
	Fec	al Coliform Bench	sheet	
Sample Location (specific Sample Type: Sample Date/Time: Collected by:	<u>GRAB</u>	Test Date: Analyst:		
Samples IN Date: Time: Oven Temp (°C)		Samples OU' Oven Temp	Time:	
Plate #	Sample Size (mLs)	# colonies on plate	Fecal coliforms per 100 mLs	Avg. Fecal coliforms per 100 mLs

colonies per plate x 100 Sample size (mL)

Calculation: Fecal coliforms per 100 mL=

Lab Equipment Maintenance and Calibration Log

Date	Analyst Intials	Sampler Temp. (°C)	Refrig. Temp. (°C)	TSS Oven Temp °C	BOD Incubator Temp °C	Fecal Incubator Temp °C	pH Meter buffers	BOD Barometer reading	BOD Room Temp °C	
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										
13										
14										
15										
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25										
26										
27										
28										
29										
30										
31										

Monthly Balance Check Monthly Balance Check			Measured weight(mg) Measured weight (g)	
Membrane changes: DO probe	Ammonia probe	Other probe		

TSS Oven should be 103-105 °C

BOD Incubator should be 20 \pm 1 C

Sampler and Refrigerator Temperature should not exceed 4° C (and samples should not be frozen)

pH calibration should be done with either a 4 and 7 buffer or a 7 and 10 buffer, depending on sample pH range. Once calibrated, one of the two buffers should be re-checked as if it was a sample. The measured pH should be within ± 0.1 pH unit of actual pH.

Corrective Action Form

TAILS WHAT IS THE LOD : W	_calibrationmatrix spikereplica What level was detected in the blank?	teblindother
	acceptance criteria? Your re	
	erference? How do you know that	
	Talue: Acceptance criteria?	
Ab b.l		
ther problems (equipment malfunctions, ymptom(s) (how did you know somethi	etc.) ing was wrong?):	
orrective Action Taken		
ist any activities or checks you performe	ed to identify the source and resolve the pro	blem.
.ction/Check Performed	What did you conclude?	Initials Date_
esolution riefly document how you know this pro	oblem has been corrected. What changes ha	Date:
riefly document how you know this pro	blem has been corrected. What changes ha	